

Amendments to the Claims:

Please amend the above-identified application, without prejudice, as follows, by amending claim 10 and adding new claim 58, set forth in the following listing of claims, which replaces all prior claims in the application:

7. (Previously Presented) A synthetic construct comprising a regulatory polynucleotide operably linked to a tandem repeat of a codon fused in frame with a reporter polynucleotide that encodes a reporter protein.
8. (Original) A vector comprising the synthetic construct of claim 7.
9. (Original) A cell comprising the synthetic construct of claim 7.
10. (Currently Amended) A cell comprising the vector of claim 9.
23. (Previously Presented) The construct of claim 7, wherein the tandem repeat comprises at least three copies of the codon.
24. (Previously Presented) The construct of claim 23, wherein the tandem repeat comprises five copies of the codon.
25. (Previously Presented) The construct of claim 23, wherein the tandem repeat comprises six copies of the codon.
26. (Previously Presented) The construct of claim 23, wherein the tandem repeat comprises seven copies of the codon.
27. (Previously Presented) The construct of claim 7, wherein the tandem repeat is fused at a location adjacent to, or within, the reporter polynucleotide.
28. (Previously Presented) The construct of claim 27, wherein the tandem repeat is fused immediately upstream of the reporter polynucleotide.
29. (Previously Presented) The construct of claim 7, wherein at least one spacer codon is located adjacent to a tandemly repeated codon.
30. (Previously Presented) The construct of claim 7, wherein at least one spacer codon is interposed between a pair of tandemly repeated codons.

31. (Previously Presented) The construct of claim 29, wherein the spacer codon is a neutral amino acid.

32. (Previously Presented) The construct of claim 30, wherein the spacer codon is a neutral amino acid.

33. (Previously Presented) The construct of claim 29, wherein the spacer codon is selected from alanine and glycine.

34. (Previously Presented) The construct of claim 30, wherein the spacer codon is selected from alanine and glycine.

35. (Previously Presented) The construct of claim 7, wherein the reporter protein is selected from the group consisting of β -galactosidase, firefly luciferase, alkaline phosphatase, chloramphenicol acetyl transferase, β -glucuronidase, green fluorescence protein and active portions thereof.

36. (Previously Presented) The construct of claim 7, wherein the reporter protein is encoded by a bialaphos resistance gene that confers resistance to the herbicide BASTA.

37. (Previously Presented) The construct of claim 7, wherein the reporter protein is green fluorescence protein or an active portion thereof.

38. (Previously Presented) A synthetic construct system for determining the translational efficiencies of different codons, the system comprising a plurality of synthetic constructs, each comprising a regulatory polynucleotide operably linked to a tandem repeat of a codon fused in frame with a reporter polynucleotide that encodes a reporter protein, wherein the tandemly repeated codon of a first construct is different than the tandemly repeated codon of a second construct.

39. (Previously Presented) The system of claim 38, wherein the tandemly repeated codons of the first and second constructs encode the same amino acid.

40. (Previously Presented) The system of claim 38, wherein the tandemly repeated codons of the first and second constructs encode different amino acids.

41. (Previously Presented) The system of claim 39, comprising a set of synthetic constructs, the number of synthetic constructs of the set being equal to the number of synonymous codons that encode a first amino acid, wherein the tandemly repeated codon of each synthetic construct of the set is a synonymous codon that encodes the first amino acid and wherein different synthetic constructs of the set comprise different tandemly repeated codons.

42. (Previously Presented) The system of claim 39, comprising a first set of synthetic constructs and a second set of synthetic constructs, the number of synthetic constructs of the first set being equal to the number of synonymous codons that encode a first amino acid, the number of synthetic constructs of the second set being equal to the number of synonymous codons that encode a second amino acid, wherein the tandemly repeated codon of each synthetic construct of the first set is a synonymous codon that encodes the first amino acid, wherein the tandemly repeated codon of each synthetic construct of the second set is a synonymous codon that encodes the second amino acid and wherein different synthetic constructs of the first or second sets comprise different tandemly repeated codons.

43. (Previously Presented) The system of claim 38, wherein the tandem repeat of each of the synthetic constructs comprises at least three copies of the corresponding codon.

44. (Previously Presented) The system of claim 43, wherein the tandem repeat of each of the synthetic constructs comprises five copies of the corresponding codon.

45. (Previously Presented) The system of claim 43, wherein the tandem repeat of each of the synthetic constructs comprises six copies of the corresponding codon.

46. (Previously Presented) The system of claim 43, wherein the tandem repeat of each of the synthetic constructs comprises seven copies of the corresponding codon.

47. (Previously Presented) The system of claim 38, wherein the tandem repeat is fused at a location adjacent to, or within, the reporter polynucleotide.

48. (Previously Presented) The system of claim 47, wherein the tandem repeat is fused immediately upstream of the reporter polynucleotide.

49. (Previously Presented) The system of claim 38, wherein at least one spacer codon is located adjacent to a tandemly repeated codon.

50. (Previously Presented) The system of claim 38, wherein at least one spacer codon is interposed between a pair of tandemly repeated codons.

51. (Previously Presented) The system of claim 49, wherein the spacer codon is a neutral amino acid.

52. (Previously Presented) The system of claim 50, wherein the spacer codon is a neutral amino acid.

53. (Previously Presented) The system of claim 49, wherein the spacer codon is selected from alanine and glycine.

54. (Previously Presented) The system of claim 50, wherein the spacer codon is selected from alanine and glycine.

55. (Previously Presented) The system of claim 38, wherein the reporter protein is selected from the group consisting of β -galactosidase, firefly luciferase, alkaline phosphatase, chloramphenicol acetyl transferase, β -glucuronidase, green fluorescence protein and active portions thereof.

56. (Previously Presented) The system of claim 38, wherein the reporter protein is encoded by a bialophos resistance gene that confers resistance to the herbicide BASTA.

57. (Previously Presented) The system of claim 38, wherein the reporter protein is green fluorescence protein or an active portion thereof.

58. (New) The construct of claim 7, wherein there are five tandemly repeated codons, the tandemly repeated codons are located immediately upstream of the reporter polynucleotide, at least one spacer codon is interspersed between a pair of tandemly repeated codons and the spacer codon is alanine.